

FIGURE 1A

1 CGCGGGGTGT TCTGGTGTCC CCCGCCCCGC CTCTCCAAAA AGCTACACCG ACGCGGACCG  
GCGCCCCACA AGACCACAGG GGGCGGGGCG GAGAGGTTTT TCGATGTGGC TCGCCTGGC

ssuI

61 CGGCGGCGTC CTCCCTCGCC CTCGCTTCAC CTCGCGGGCT CCGAATGCGG GGAGCTCGGA  
GCCGCCGAG GAGGGAGCGG GAGCGAAGTG GAGCGCCCGA GGCTTACGCC CCTCGAGCCT

121 TGTCCGGTTT CCTGTGAGGC TTTTACCTGA CACCCGCCGC CTTTCCCCGG CACTGGCTGG  
ACAGGCCAAA GGACACTCCG AAAATGGACT GTGGGCGGCG GAAAGGGGCC GTGACCGACC

kasI

181 GAGGGCGCCC TGCAAAGTTG GGAACGCGGA GCGCCGACC CGCTCCCGCC GCCTCCGGCT  
CTCCGCGGGG ACGTTTCAAC CCTTGCGCCT CGGGGCTGG GCGAGGGCGG CGGAGGCCGA

241 CGCCCAGGGG GGGTCGCCGG GAGGAGCCCG GGGGAGAGGG ACCAGGAGGG GCGCGCGGCC  
GCGGGTCCCC CCCAGCGGCC CTCCTCGGGC CCCCTCTCCC TGGTCCTCCC CGGGCGCCGG

kasI

ageI

301 TCGCAGGGGC GCGCGCGCCC CCACCCCTGC CCGCGCCAGC GGACCGGTCC CCCACCCCGG  
AGCGTCCCCG CGGGCGCGGG GGTGGGGACG GGGGCGGTTCG CCTGGCCAGG GGGTGGGGGC

361 GTCCTTCAC CATGCACTTG CTGGGCTTCT TCTCTGTGGC GTGTTCTCTG CTCGCCGCTG  
CAGGAAGGTG GTACGTGAAC GACCCGAAGA AGAGACACCG CACAAGAGAC GAGCGGCGAC  
-20 M H L L G F F S V A C S L L A A A

kasI

421 CGCTGCTCCC GGGTCCTCGC GAGGCGCCCC CCGCGCCGC CGCCTTCGAG TCCGGAAGTCG  
GCGACGAGGG CCCAGGAGCG CTCCGCGGGC GCGGCGGGC GCGGAAGCTC AGGCCTGAGC  
-3 L L P G P R E A P A A A A F E S G L D

481 ACCTCTCGGA CGCGGAGCCC GACGCGGGCG AGGCCACGGC TTATGCAAGC AAAGATCTGG  
TGGAGAGCCT GCGCCTCGGG CTGCGCCCGC TCCGGTGCCG AATACGTTTCG TTTCTAGAGC  
18 L S D A E P D A G E A T A Y A S K D L E

541 AGGAGCAGTT ACGGTCTGTG TCCAGTGTAG ATGAACTCAT GACTGTACTC TACCCAGAAT  
TCCTCGTCAA TGCCAGACAC AGGTCACATC TACTTGAGTA CTGACATGAG ATGGGTCTTA  
38 E Q L R S V S S V D E L M T V L Y P E Y

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FIGURE 1B

601 ATTGGAAAAT GTACAAGTGT CAGCTAAGGA AAGGAGGCTG GCAACATAAC AGAGAACAGG  
 TAACCTTTTA CATGTTTACA GTCGATTCTT TTCCTCCGAC CGTTGTATTG TCTCTTGTCC  
 58 W K M Y K C Q L R K G G W Q H N R E Q A

661 CCAACCTCAA CTCAAGGACA GAAGAGACTA TAAATTTGC TGCAGCACAT TATAATACAG  
 GGTGGAGTT GAGTTCCTGT CTTCTCTGAT ATTTTAAACG ACGTCGTGTA ATATTATGTC  
 78 N L N S R T E E T I K F A A A H T N T E

sphI

721 AGATCTTGAA AAGTATTGAT AATGAGTGGG GAAAGACTCA ATGCATGCCA CGGGAGGTGT  
 TCTAGAACTT TTCATACTA TTACTCACCT CTTTCTGAGT TACGTACGGT GCCCTCCACA  
 98 I L K S I D N E W R K T Q C M P R E V C

781 GTATAGATGT GGGGAAGGAG TTTGGAGTCG CGACAAACAC CTTCTTTAAA CCTCCATGTG  
 CATATCTACA CCCCTTCCTC AAACCTCAGC GCTGTTTGTG GAAGAAATTT GGAGGTACAC  
 118 I D V G K E F G V A T N T F F K P P C V

accI

841 TGTCCGTCTA CAGATGTGGG GGTGCTGCA ATAGTGAGGG GCTGCAGTGC ATGAACACCA  
 ACAGGCAGAT GTCTACACCC CCAACGACGT TATCACTCCC CGACGTCACG TACTTGTGGT  
 138 S V Y R C G G C C N S E G L Q C M N T S

901 GCACGAGCTA CCTCAGCAAG ACGTTATTTG AAATTACAGT GCCTCTCTCT CAAGGCCCCA  
 CGTGCTCGAT GGAGTCGTTT TGCAATAAAC TTTAATGTCA CGGAGAGAGA GTTCCGGGGT  
 158 T S Y L S K T L F E I T V P L S Q G P K

961 AACCAGTAAC AATCAGTTTT GCCAATCACA CTTCCTGCCG ATGCATGTCT AAACCTGGATG  
 TTGGTCATTG TTAGTCAAAA CGGTTAGTGT GAAGGACGGC TACGTACAGA TTTGACCTAC  
 178 P V T I S F A N H T S C R C M S K L D V

1021 TTTACAGACA AGTTCATTCC ATTATTAGAC GTTCCCTGCC AGCAACACTA CCACAGTGTC  
 AAATGTCTGT TCAAGTAAGG TAATAATCTG CAAGGGACGG TCGTTGTGAT GGTGTCACAG  
 198 Y R Q V H S I I R R S L P A T L P Q C Q

1081 AGGCAGCGAA CAAGACCTGC CCCACCAATT ACATGTGGAA TAATCACATC TGCAGATGCC  
 TCCGTCGCTT GTTCTGGACG GGGTGGTTAA TGTACACCTT ATTAGTGTAG ACGTCTACGG  
 218 A A N K T C P T N Y M W N N H I C R C L

601  
661  
721  
781  
841  
901  
961  
1021  
1081

FIGURE 1C

1141 TGGCTCAGGA AGATTTTATG TTTTCCTCGG ATGCTGGAGA TGA CTCAACA GATGGATTCC  
ACCGAGTCCT TCTAAAATAC AAAAGGAGCC TACGACCTCT ACTGAGTTGT CTACCTAAGG  
238 A Q E D F M F S S D A G D D S T D G F H

1201 ATGACATCTG TGGACCAAAC AAGGAGCTGG ATGAAGAGAC CTGTCA GTGT GTCTGCAGAG  
TACTGTAGAC ACCTGGTTTG TTCCTCGACC TACTTCTCTG GACAGTCACA CAGACGTCTC  
258 D I C G P N K E L D E E T C Q C V C R A

1261 CGGGGCTTCG GCCTGCCAGC TGTGGACCCC ACAAAGA AACT AGACAGAAAC TCATGCCAGT  
GCCCCGAAGC CGGACGGTCG ACACCTGGGG TGTTCCTTGA TCTGTCTTTG AGTACGGTCA  
278 G L R P A S C G P H K E L D R N S C Q C

1321 GTGTCTGTAA AAACAACTC TTCCCCAGCC AATGTGGGGC CAACCGAGAA TTTGATGAAA  
CACAGACATT TTTGTTTGAG AAGGGGTCGG TTACACCCCG GTTGGCTCTT AAAC TACTTT  
298 V C K N K L F P S Q C G A N R E F D E N

1381 ACACATGCCA GTGTGTATGT AAAAGAACCT GCCCCAGAAA TCAACCCCTA AATCCTGGAA  
TGTGTACGGT CACACATACA TTTTCTTGGA CGGGGTCTTT AGTTGGGGAT TTAGGACCTT  
318 T C Q C V C K R T C P R N Q P L N P G K

1441 AATGTGCCTG TGAATGTACA GAAAGTCCAC AGAAATGCTT GTTAAAAGGA AAGAAGTTCC  
TTACACGGAC ACTTACATGT CTTTCAGGTG TCTTTACGAA CAATTTTCCT TTCTTCAAGG  
338 C A C E C T E S P Q K C L L K G K K F H

eaeI

1501 ACCACCAAAC ATGCAGCTGT TACAGACGGC CATGTACGAA CCGCCAGAAG GCTTGTGAGC  
TGGTGGTTTG TACGTCGACA ATGTCTGCCG GTACATGCTT GGCGGTCTTC CGAACACTCG  
358 H Q T C S C Y R R P C T N R Q K A C E P

1561 CAGGATTTTC ATATAGTGAA GAAGTGTGTC GTTGTGTCCC TTCATATTGG AAAAGACCAC  
GTCCTAAAAG TATATCACTT CTTACACAG CAACACAGGG AAGTATAACC TTTTCTGGTG  
378 G F S Y S E E V C R C V P S Y W K R P Q

clal

1621 AAATGAGCTA AGATTGTACT GTTTTCCAGT TCATCGATTT TCTATTATGG AAAACTGTGT  
TTTACTCGAT TCTAACATGA CAAAAGGTCA AGTAGCTAAA AGATAATACC TTTTGACACA  
398 M S O

1681 TGCCACAGTA GAACTGTCTG TGAACAGAGA GACCCTTGTG GGTCCATGCT AACAAAGACA  
ACGGTGT CAT CTTGACAGAC ACTTGTCTCT CTGGGAACAC CCAGGTACGA TTGTTTCTGT

FIGURE 1D

sstI

1741 AAAGTCTGTC TTTCTGAAC CATGTGGATA ACTTTACAGA AATGGACTGG AGCTCATCTG  
TTTCAGACAG AAAGGACTTG GTACACCTAT TGAAATGTCT TTACCTGACC TCGAGTAGAC

1801 CAAAAGGCCT CTTGTAAAGA CTGGTTTTCT GCCAATGACC AAACAGCCAA GATTTTCCTC  
GTTTTCCGGA GAACATTTCT GACCAAAGA CGTTACTGG TTTGTCGGTT CTAAAAGGAG

1861 TTGTGATTTC TTTAAAAGAA TGACTATATA ATTTATTTCC ACTAAAATA TTGTTTCTGC  
AACACTAAAG AAATTTTCTT ACTGATATAT TAAATAAAGG TGATTTTAT AACAAAGACG

1921 ATTCATTTTT ATAGCAACAA CAATTGGTAA AACTCACTGT GATCAATATT TTTATATCAT  
TAAGTAAAAA TATCGTTGTT GTTAACCATT TTGAGTGACA CTAGTTATAA AAATATAGTA

1981 GCAAAATATG TTTAAAATAA AATGAAATT GTATTAAAAA AAAAAAAAAA A  
CGTTTTATAC AAATTTTATT TTACTTTTAA CATAATTTTT TTTTTTTTTT T

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002450-6626160

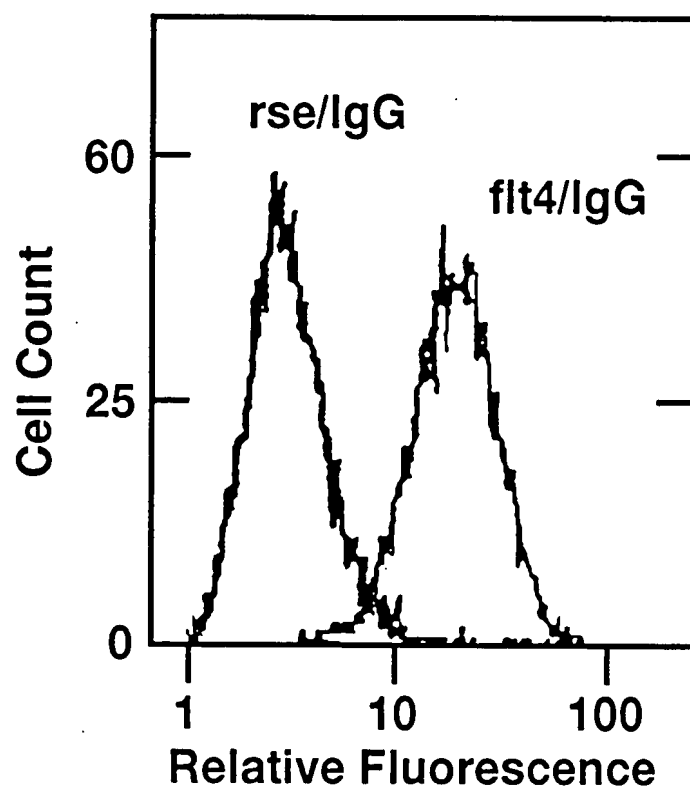
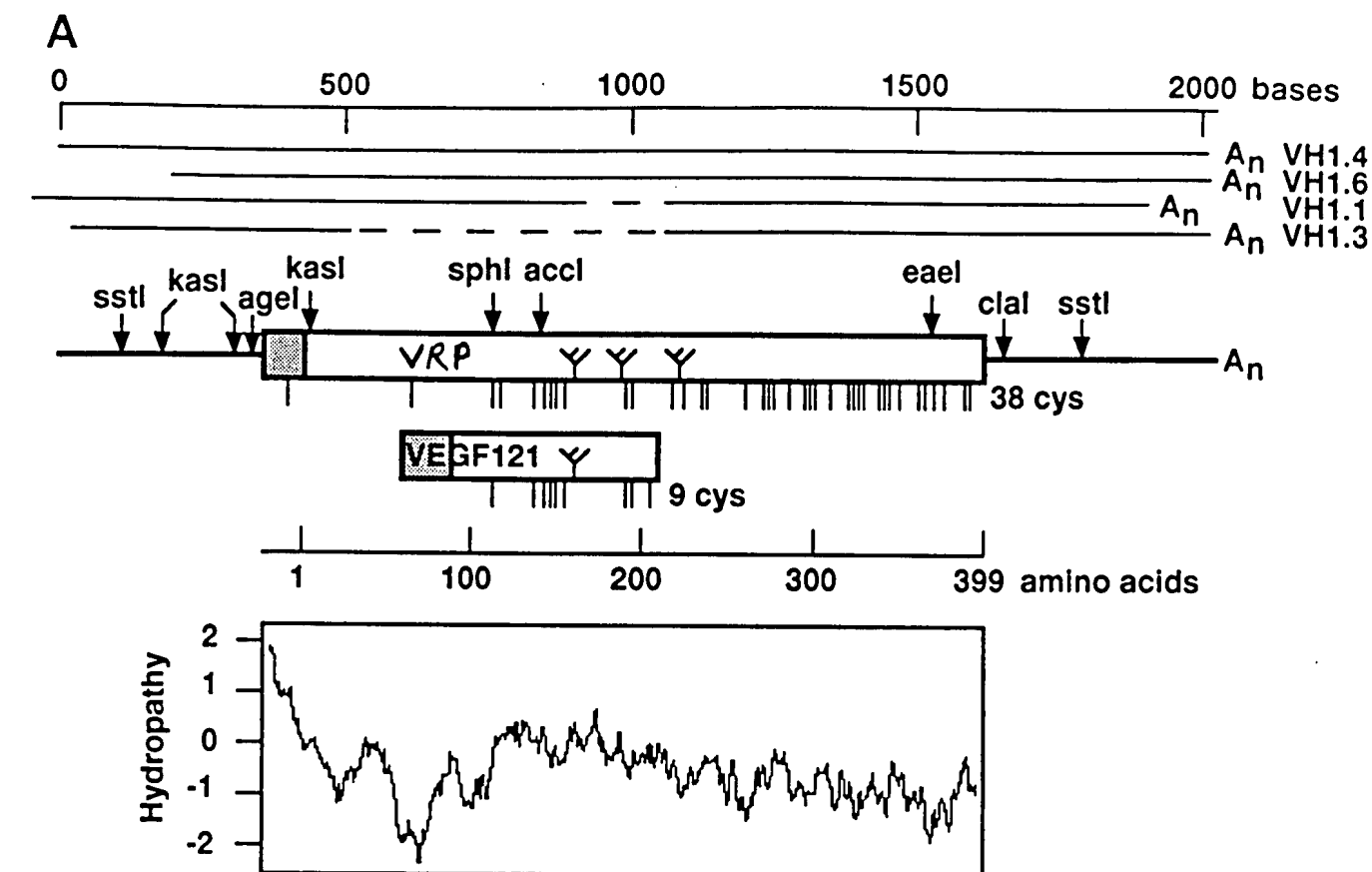


Figure 2



**B**

VRP	-20	MHLLGFFSVACSLLAALLPGPREAPAAAAAFESGLDLSDAEPDAGEATA
VRP	31	YASKDLEEQLRSVSSVDELMTVLYPEYWKMYKCLRKGGWQHNRQAANLN
VEGF121	-26	.....MNFLLSWVHWSLALLLYLHHA
PIGF131	-18	.....MPVMRLFPCLQLLAGLALPA
VRP	81	SRTEETIKFAAAHYNTEILKSIDNEWRKTQCMPREVCIDVGKEFGVATNT
VEGF121	-5	KWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVDIFOEYPDEIEY
PIGF131	4	VPPQQWALSAGNGSSEVEVVPFQEVWGRSYCRALERLVDVVS EYPS EVEH
VRP	131	FFKPPCVSVYRCGGCCNSEGLQCMNTSTSYLSKTLEFII TVPLSOGPKPVT
VEGF121	46	IFKPSCVPLMRCCGGCCNDEGLECVPTTEESNITMQIMRIKP--HGGHIGE
PIGF131	54	MFSPSCVSLLRCTGCCGDENLHCVPVETANVTMQLLKIRS--GDRPSYVE
VRP	181	ISFANHTSCRCMSKLDVYRQVHSIIRRS L PATLPQCAANKTCPTNYMWN
VEGF121	94	MSFLQHNKCECRPKKDRARQEKCDKPRR
PIGF131	102	LTFSQHVRCECRPLREKMKPERCGDAVPRR
VRP	231	NHICRCLAQEDFMFSSDAGDDSTDGFHDICGPNKELDEETCQCVCRAGLR
VRP	281	PASCGPHKELDRNSCQCVCKNKLFPSCGANREFDENTCQCVCKRTCPRN
VRP	331	QPLNPGKCAECTESPQKCLLKGKKFHHOTCSCYRRPCTNRQKACEPGFS
VRP	381	YSEEVCRVCVPSYWKRPQMS

Figure 3

# Contig[0002] Sequencher™ "Untitled Project"

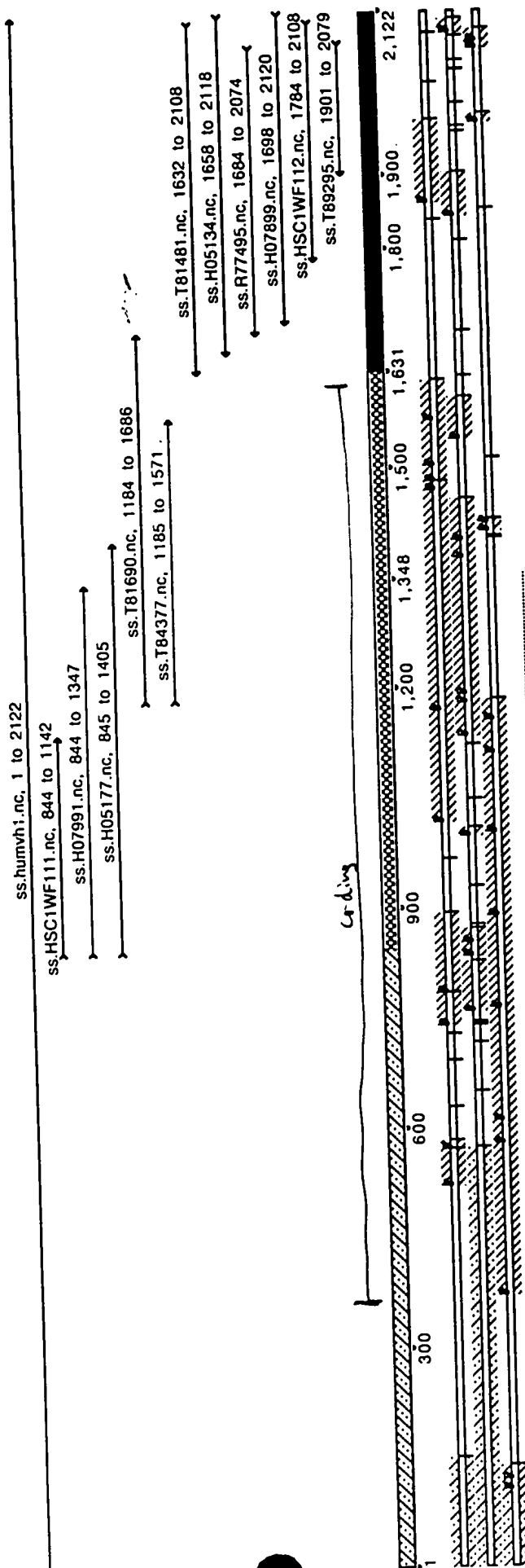


Diagram Key	
	Hole in contig
	Single fragment
	Multiple fragments same direction
	Both strands
	Both strands plus
	Start codon frame 1
	Stop codon frame 2
	Bumps on fragments
	show motifs, hollow rectangles
	show features

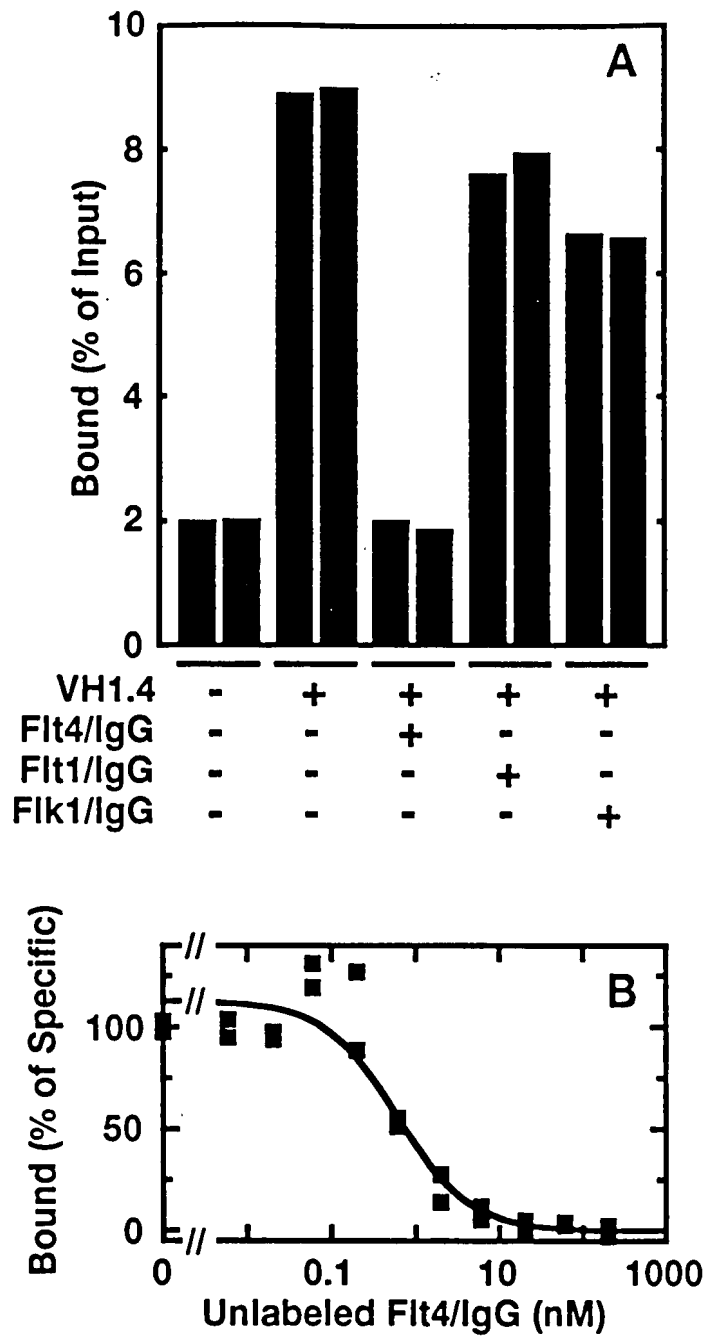


Figure 5



FIG. 6

